

**STIC Biotechnology Systems Branch**

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/537,746

Source: PCH

Date Processed by STIC: 6/14/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

## RAW SEQUENCE LISTING

DATE: 06/14/2005

PATENT APPLICATION: US/10/537,746

TIME: 09:17:55

Input Set : A:\01-SQ Listing-06 Jun 2005.txt

Output Set: N:\CRF4\06142005\J537746.raw

3 <110> APPLICANT: De Maria, Leonardo  
 4 Svendsen, Allan  
 5 Borchert, Torben Vedel  
 6 Christensen, Lars Lehmann Hylling  
 7 Larsen, Sine  
 8 Ryttergaard, Carsten  
 10 <120> TITLE OF INVENTION: Galactanase Variants  
 12 <130> FILE REFERENCE: 10319.204-US  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/537,746  
 C--> 14 <141> CURRENT FILING DATE: 2005-06-06  
 14 <160> NUMBER OF SEQ ID NOS: 9  
 16 <170> SOFTWARE: PatentIn version 3.3

Does Not Comply  
 Corrected Diskette Needed

(Pg. 2-3)

## ERRORED SEQUENCES

645 <210> SEQ ID NO: 9  
 646 <211> LENGTH: 359  
 647 <212> TYPE: PRT  
 648 <213> ORGANISM: Pseudomonas fluorescens  
 651 <220> FEATURE:  
 652 <221> NAME/KEY: mat\_peptide  
 653 <222> LOCATION: (1)..()  
 655 <400> SEQUENCE: 9  
 657 Asn Thr Gly Val Ala Asp Asn Thr Pro Phe Tyr Val Gly Ala Asp Leu  
 658 1 5 10 15  
 661 Ser Tyr Val Asn Glu Met Glu Ser Cys Gly Ala Thr Tyr Arg Asp Gln  
 662 20 25 30  
 665 Gly Lys Lys Val Asp Pro Phe Gln Leu Phe Ala Asp Lys Gly Ala Asp  
 666 35 40 45  
 669 Leu Val Arg Val Arg Leu Trp His Asn Ala Thr Trp Thr Lys Tyr Ser  
 670 50 55 60  
 673 Asp Leu Lys Asp Val Ser Lys Thr Leu Lys Arg Ala Lys Asn Ala Gly  
 674 65 70 75 80  
 677 Met Lys Thr Leu Leu Asp Phe His Tyr Ser Asp Thr Trp Thr Asp Pro  
 678 85 90 95  
 681 Glu Lys Gln Phe Ile Pro Lys Ala Trp Ala His Ile Thr Asp Thr Lys  
 682 100 105 110  
 685 Glu Leu Ala Lys Ala Leu Tyr Asp Thr Thr Asp Thr Leu Ala Ser  
 686 115 120 125  
 689 Leu Asp Gln Gln Gln Leu Leu Pro Asn Leu Val Gln Val Gly Asn Glu  
 690 130 135 140  
 693 Thr Asn Ile Glu Ile Leu Gln Ala Glu Asp Thr Leu Val His Gly Ile

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/537,746

DATE: 06/14/2005

TIME: 09:17:55

Input Set : A:\01-SQ Listing-06 Jun 2005.txt

Output Set: N:\CRF4\06142005\J537746.raw

694 145 150 155 160  
697 Pro Asn Trp Gln Arg Asn Ala Thr Leu Leu Asn Ser Gly Val Asn Ala  
698 165 170 175  
701 Val Arg Asp Tyr Ser Lys Lys Thr Gly Lys Pro Ile Gln Val Val Leu  
702 180 185 190  
705 His Ile Ala Gln Pro Glu Asn Ala Leu Trp Trp Phe Lys Gln Ala Lys  
706 195 200 205  
709 Glu Asn Gly Val Ile Asp Tyr Asp Val Ile Gly Leu Ser Tyr Tyr Pro  
710 210 215 220  
713 Gln Trp Ser Glu Tyr Ser Leu Pro Gln Leu Pro Asp Ala Ile Ala Glu  
714 225 230 235 240  
717 Leu Gln Asn Thr Tyr His Lys Pro Val Met Ile Val Glu Thr Ala Tyr  
718 245 250 255  
721 Pro Trp Thr Leu His Asn Phe Asp Gln Ala Gly Asn Val Leu Gly Glu  
722 260 265 270  
725 Lys Ala Val Gln Pro Glu Phe Pro Ala Ser Pro Arg Gly Gln Leu Thr  
726 275 280 285  
729 Tyr Leu Leu Thr Leu Thr Gln Leu Val Lys Ser Ala Gly Gly Met Gly  
730 290 295 300  
733 Val Ile Tyr Trp Glu Pro Ala Trp Val Ser Thr Arg Cys Arg Thr Leu  
734 305 310 315 320  
737 Trp Gly Lys Gly Ser His Trp Glu Asn Ala Ser Phe Phe Asp Ala Thr  
738 325 330 335  
741 Arg Lys Asn Asn Ala Leu Pro Ala Phe Leu Phe Phe Lys Ala Asp Tyr  
742 340 345 350  
745 Gln Ala Ser Ala Gln Ala Glu  
746 355

E--&gt;

752 1

*pls delete*

10/ 537,746

Page 3

<210> 5  
<211> 21  
<212> DNA  
<213> synthetic

Invalid  
Response

<220>  
<221> misc\_feature  
<223> Primer

<400> 5  
catttgga caggctggag c

← Mandatory,

<213> response 21  
has to be either  
Artificial,  
Unknown or  
Genus / species,

↑  
pls see  
item # 10  
on error  
summary sheet

↑  
The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

## VERIFICATION SUMMARY

DATE: 06/14/2005

PATENT APPLICATION: US/10/537,746

TIME: 09:17:56

Input Set : A:\01-SQ Listing-06 Jun 2005.txt

Output Set: N:\CRF4\06142005\J537746.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:752 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/537,746

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4        Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5        Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7        Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
                               (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                               (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               This sequence is intentionally skipped  
  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence.  
                               <210> sequence id number  
                               <400> sequence id number  
                               000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                               Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                               In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10        Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11        Use of <220>     Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses.  
                               Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                               (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12        PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa     "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid